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Development of diagnostic markers and physical mapping for the *Rrs1* resistance locus against scald

Büttner B (1), Silvar C (2), Casas A (2), Igartua E (2), Mayer K (3), Schweizer G (1)

(1) Bavarian State Research Center for Agriculture, Institute for Crop Science and Plant Breeding, Am Gereuth 2, 85354 Freising, Germany

(2) Aula Dei Experimental Station, CSIC, Department of Genetics and Plant Production, Av. Montanana, 1005, 50059 Zaragoza, Spain

(3) Munich Information Centre for Protein Sequences, Institute for Bioinformatics and Systems Biology, Helmholtz Zentrum München, Ingolstädter Landstrasse 1, 85764 Neuherberg, Germany

Contact: Bianca.Buettner@lfl.bayern.de or Guenther.Schweizer@lfl.bayern.de

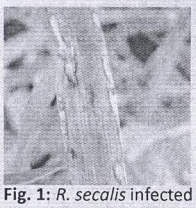

Fig. 1: *R. secalis* infected leaf 21 days after inoculation

INTRODUCTION

***Rhynchosporium secalis*, the causal agent of scald, is still one of the most important foliar diseases of barley. Its high genetic variability and recombination frequency enable it to rapidly overcome monogenic resistances. To date four major scald resistance genes have been identified in cultivated barley (*Hordeum vulgare* ssp. *vulgare*), and another four in wild barley (*Hv. spontaneum* or *Hv. bulbosum*). The most abundant and effective one is the *Rrs1* resistance locus, mapping near the centromeric region of chromosome 3H. Aim of the project is the fine mapping of the *Rrs1* locus and the development of diagnostic markers.**

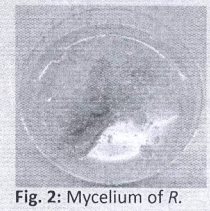

Fig. 2: Mycelium of *R. secalis*

MATERIAL and METHODS

Resistance to *Rhynchosporium secalis* was detected in the Spanish landraces SBCC145 and SBCC154 (Tab.1; Silvar et al., 2010). A DH population of 523 lines from the cross SBCC145 with the susceptible parent Beatrix was constructed and rated for resistance in the field and greenhouse. A QTL analysis was conducted with two different isolates of *R. secalis* (271, LfL07). The resistance locus *Rrs1* on chromosome 3H has been saturated with markers and new markers are developed based on the Illumina iSelect custom 9K barley chip, the barley Genome Zipper and a bulked segregant analysis (BSA) with AFLP. For gene isolation a high resolution mapping population comprising 10.000 F_2 plants from the cross SBCC145 x Beatrix has been constructed.

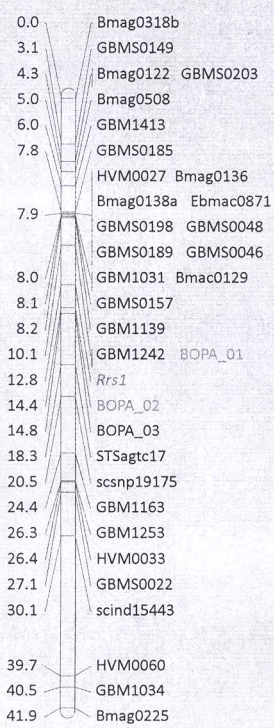

Fig. 2: Map of chromosome 3H DH population SBCC145 x Beatrix

Tab. 1: Rating scores for the resistance donors and susceptible parent after inoculation with eight different single spore isolates. 0 stands for full resistance (no symptoms), 4 for highly susceptible.

	271	S 147-1	Rhy17	Rhy174	SGü 4/3	UK7	AU2	LfL07
Beatrix	4,00	4,00	4,00	3,75	4,00	4,00	4,00	4,00
SBCC145	0,00	0,00	0,00	0,19	0,00	0,25	0,00	0,00
SBCC154	0,00	0,00	0,00	0,00	0,00	0,00	0,00	0,00

RESULTS

The DH population SBCC145 x Beatrix was phenotyped for scald resistance in a well established greenhouse test, and sub-populations were tested under field conditions. The segregation ratio suggested one major resistance gene being responsible for resistance.

The QTL analysis detected a single QTL on chromosome 3H and therefore confirmed this locus as the only resistance locus in this population (Fig.1).

A map of the *Rrs1* locus was constructed (Fig.2). The Illumina iSelect custom 9K barley chip identified no new polymorphic marker in the interval between the *Rrs1* flanking markers. The *Rrs1* flanking markers were identified in the Genome Zipper (Mayer et al., 2009; Close et al., 2009) and 64 candidate genes were identified between them. Sequence analysis and mapping of the candidates is in progress.

A BSA-AFLP approach led to six fragments, which clearly differentiate between susceptible and resistant DNA-pools (Fig.3) and could be validated in single plants. These fragments are now used for marker development.

F_2 screening of about 7200 plants to select recombinant lines between two flanking markers has identified 390 recombinant plants (Tab.2), screening of the remaining plants is in progress.

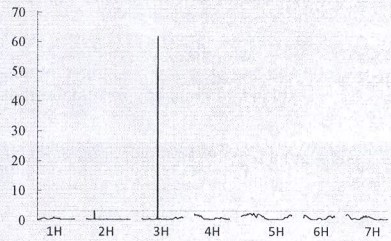

Fig. 1: QTL analysis of DH population SBCC145 x Beatrix with *R. secalis* isolate LfL07. The analysis showed one distinct QTL on chromosome 3H.

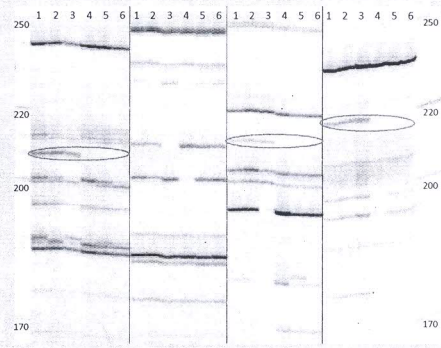

Fig. 3: BSA with AFLP, excerpt of PAA gel
line 1 and 2 pool of 5 resistant plants each; line 3 resistant parent; line 4 susceptible parent, line 5 and 6 pool of 5 susceptible plants

Tab. 2: Segregation of recombinant F_2 plants

BOPA_01	cc[1]	bb	bc	bb	bc	cc
BOPA_02	bb[2]	cc	bb	bc	cc	bc
No. F_2 plants	11	12	80	134	92	61

[1] Allele of Beatrix (susceptible), [2] allele of SBCC145 (resistant)

Literature:

Silvar et al., Plant Breeding, 2010, 129(1): 45-52

Mayer et al., Plant Physiology, 2009, 151(2): 496-505

Close et al., BMC Genomics, 2009, 10: 582

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PLANT 2030 Status Seminar

March 6-8 2013, Potsdam Germany

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PLANT 2030 Status Seminar 2013

Potsdam from March 6 - 8, 2013

The PLANT2030 Status Seminar 2013 will take place in Potsdam from March 6 - 8, 2013. As in 2012, venue is the Kongresshotel Potsdam on the shore of Lake Templin. The agenda will include presentations on the progress made in running Plant Biotechnology, PLANT KBBE, and related projects. Poster session will be held for all sub projects and prices for the best posters will be awarded.

Some features of this website including abstracts, comments and a list of participants are only available to registered attendees of the meeting. If you are logged in with your personal account you gain access to these features. All data presented until end of January are preliminary, please ensure that you keep an eye on updates regularly.

Registration ▸ (/registration)

Who may participate?

The Status Seminar is an internal conference and not open to the public. Therefore please check if you are eligible for attending the conference.

Attendance compulsory
Each principal investigator (PI) of ongoing PLANT 2030 related (sub-) projects (i.e. Plant Biotechnology, PLANT KBBE, GABI FUTURE) **has to** participate and present the progress made in the respective projects. If you are not able to attend the seminar personally you must find a substitute.

Attendance encouraged
Scientists (Post-docs, PhD-Students etc.) involved in the abovementioned PLANT 2030 projects are welcome to attend the seminar. They are strongly encouraged to present their work on a poster. Members of former GABI, PLANT KBBE or ERA-Net PG projects are also welcome to join the seminar.
Participants in other plant-related projects like BioEnergy 2021 or AgroClustEr are invited to take part in the seminar. Poster presentations on the projects are highly appreciated.